L1 ANSWER 9 OF 139 MEDLINE
AN 2002365511 MEDLINE
DN 22103463 PubMed ID: 12107413
TI Expressed sequence tag analysis of adult human lens for the NEIBank Project: over 2000 non-redundant transcripts, novel genes and splice variants.
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SO MOLECULAR VISION, (2002 Jun 15) 8 171-84.
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DT Journal; Article; (JOURNAL ARTICLE)
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AB PURPOSE: To explore the expression profile of the human lens and to provide a resource for microarray studies, expressed sequence tag (EST) analysis has been performed on cDNA libraries from adult lenses. METHODS: A cDNA library was constructed from two adult (40 year old) human lenses. Over two thousand clones were sequenced from the unamplified, un-normalized library. The library was then normalized and a further 2200 sequences were obtained. All the data were analyzed using GRIST (GRouping and Identification of Sequence Tags), a procedure for gene identification and clustering. RESULTS: The lens library (by) contains a low percentage of non-mRNA contaminants and a high fraction (over 75%) of apparently full length cDNA clones. Approximately 2000 reads from the unamplified library yields 810 clusters, potentially representing individual genes expressed in the lens. After normalization, the content of crystallins and other abundant cDNAs is markedly reduced and a similar number of reads from this library (fs) yields 1455 unique groups of which only two thirds correspond to named genes in GenBank. Among the most abundant cDNAs is one for a novel gene related to glutamine synthetase, which was designated "lengsin" (LGS). Analyses of ESTs also reveal examples of alternative transcripts, including a major alternative splice form for the lens specific membrane protein MP19. Variant forms for other transcripts, including those encoding the apoptosis inhibitor Livin and the armadillo repeat protein ARVCF, are also described. CONCLUSIONS: The lens cDNA libraries are a resource for gene discovery, full length cDNAs for functional studies and microarrays. The discovery of an abundant, novel transcript, lengsin, and a major novel splice form of MP19 reflect the utility of unamplified libraries constructed from dissected tissue. Many novel transcripts and splice forms are represented, some of which may be candidates for **genetic diseases**.

L1 ANSWER 2 OF 2 MEDLINE
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TI Localization of a FITC-labeled phosphorothioate oligodeoxynucleotide in the skin after topical delivery by **iontophoresis** and electroporation.
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AB PURPOSE: The aim of this study was to verify the hypothesis that the application of high voltage to the skin enhances both stratum corneum and keratinocyte permeability. Therefore, the transport of FITC labelled phosphorothioate oligonucleotides (FITC-PS) administered by passive diffusion, **iontophoresis** or electroporation was localized. METHODS: Fluorescent microscopy and laser scanning confocal microscopy were used to visualize the FITC-PS transport at the tissue and cell level respectively in hairless rat skin after electroporation (5 x (200 V approximately 500 ms) or **iontophoresis** (same amount of charges transferred). RESULTS: FITC-PS did not penetrate the viable skin by passive diffusion. Molecular transport in the skin upon electroporation or **iontophoresis** was localized and implied mainly hair follicles for **iontophoresis**. In the stratum corneum, the pathways for FITC-PS transport were more transcellular during electroporation and paracellular during **iontophoresis**. FITC-PS were detected in the nucleus of the keratinocytes a few minutes after pulsing. In contrast, **iontophoresis** did not lead to an uptake of the oligomer. CONCLUSIONS: The internalization of FITC-PS in the keratinocytes after electroporation confirms the hypothesis and suggests that electroporation, which allows both efficient topical delivery and rapid cellular uptake of the oligonucleotides, might be useful for **antisense** therapy of **epidermal** diseases.